To: Peters, Emily (MPCA)[Emily.Peters@state.mn.us]
From: Erickson, Russell
Sent: Sat 2/15/2014 6:32:15 PM
Subject: RE: advice on fitting new models

Sorry about not connecting on the phone – I also tried to call you yesterday at the office and on your cell a short time ago. I have also just sent a email to you, Phil, and Ed summarizing some of my thoughts on this.

Regarding your first two questions:

No, I did not intend that you force B=0, so this is still different from TRAP.

Regarding the sparse data issue:

I have only looked at the weight data, and the only real problem is with D2, For R and D1, my stat software had no problems fitting the curves and provided reasonable standard errors and similar ECs. For D2, a curve cannot be fit, because the average weight at 10uM is only slightly lower than the average at the lower treatments and at 20uM is no higher than at the higher treatment, meaning there is at most one, weak partial effect to work with. This dataset would need an interpolation approach, which has precedence in aquatic toxicology and can still reasonably bound the EC50. Each set will still have a clear relationship that is consistent with the other sets. Although doing a pooled analysis helps address the sparse D2 data, and I think your actual analysis is useful in this regard, overall I don't think it adds value and clarity to the analyses given the various complexities and uncertainties it entails for this particular dataset.

I will try to call you again this weekend, and will be in the office from 8-10 on Monday.

Russell Erickson

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From: Peters, Emily (MPCA) [mailto:Emily.Peters@state.mn.us]
Sent: Friday, February 14, 2014 3:59 PM
To: Erickson, Russell
Subject: advice on fitting new models

Russ,

I just finished chatting with Ed Swain about your concerns regarding the 4-parameter logistic modeling approach. I have a couple follow up questions for you. Just tried to call, but your line was busy. I'm in the office only a few more minutes, but feel free to call me on my call at 612-616-8688 over the weekend/Monday.

1.   You suggested fitting each test separately (not pooled) and forcing B = 0. Correct?

2.   If so, how is this different from the analyses I ran using TRAP, which instigated the pooled-data suggestion? There will be many large residuals at high sulfide values because of the negative growth rates (especially the definitive 2 test). Aren't you worried about this?

3.   Finally, I'm concerned about the sparse data coverage along the slope of the curve when fitting models separately for each test. It was a problem doing this in TRAP and I'm doubtful I'll be able to "force" the fits in R like I could in TRAP. Does this make sense?

Thanks much for your insight.

-Emily

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